SEQUENCE LISTING

<110> Salceda, Susana
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Cafferkey, Robert

<120> A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING, IMAGING AND
TREATING VARIOUS CANCERS

<130> DEX-0172

<140> 09/763,978
<141> 2001-02-28

<150> PCT/US99/19655
<151> 1999-09-01

<150> 60/098,880
<151> 1998-09-02

<160> 16

<170> PatentIn version 3.1

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atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg   2400

atgctcagtt taaggtacac tgtttccatg ttatgtttct acacattgat ggtggtgacc   2460

ctgagttcaa agccatctt                                                2479
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<210>   10
<211>   576
<212>   DNA
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<213> Homo sapien

<400> 10
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gtgataagta aaatgcacgt ggagacaagt gcatccccag atctcaggga cctcccctg   120

cctgtcacct ggggagtgag aggacaggat agtgcatgtt ctttgtctct gaatttttag   180

ttatatgtgc tgtaatgttg ctctgaggaa gccctggaa agtctatccc aacatatcca   240

catcttatat tccacaaatt aagctgtagt atgtaccta agacgctgct aattgactgc   300

cacttcgcaa ctcaggggcg gctgcatttt agtaatgggt caaatgattc actttttatg   360

atgcttccaa aggtgccttg gcttctcttc ccaactgaca aatgccaaag ttgagaaaaa   420

tgatcataat tttagcataa acagagcagt cggcgacacc gattttataa ataaactgag   480

caccttcttt ttaaacaaac aaatgcgggt ttatttctca gatgatgttc atccgtgaat   540

ggtccaggga aggacctttc accttgacta tatggc   576

<210> 11
<211> 890
<212> DNA
<213> Homo sapien

<400> 11
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gcatctagag cagtgggact cagctggggt gatttcgccc cccatctccg ggggaatgtc   120

tgaagacaat tttggttacc tcaatgaggg agtggaggag gatacagtgc tactaccaac   180

tagtggataa aggccaggga tgctgctcaa cctcctacca tgtacaggga cgtctcccca   240

ttacaactac ccaatccgaa gtgtcaactg tgtcaggact aagaaaccct ggttttgagt   300

agaaaagggc ctggaaagag gggagccaac aaatctgtct gcttcctcac attagtcatt   360

ggcaaataag cattctgtct ctttggctgc tgcctcagca cagagagcca gaactctatc   420

gggcaccagg ataacatctc tcagtgaaca gagttgacaa ggcctatggg aaatgcctga   480

tgggattatc ttcagcttgt tgagcttcta gtttctttc ccttcattct accctgcaag   540

ccaagttctg taagagaaat gcctgagttc tagctcaggt tttcttactc tgaatttaga   600

tctccagacc cttcctggcc acaattcaaa ttaaggcaac aaacatatac cttccatgaa   660

gcacacacag acttttgaaa gcaaggacaa tgactgcttg aattgaggcc ttgaggaatg   720

aagctttgaa ggaaaagaat actttgtttc cagcccccctt cccacactct tcatgtgtta   780

accactgcct tcctggacct tggagccacg gtgactgtat tacatgttgt tatagaaaac   840

tgattttaga gttctgatcg ttcaagagaa tgattaaata tacatttcct   890

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<210>  12
<211>  406
<212>  DNA
<213>  Homo sapien

<220>
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<222>  (30)..(30)
<223>  n= a, c, g, or t


<220>
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<222>  (248)..(248)
<223>  n= a, c, g, or t


<220>
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<222>  (383)..(383)
<223>  n= a, c, g, or t


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tccaatacca gctttgagct gaactctgag aatgtgacca tgaaggttgt gtctgtgctc       180

tacaatgtta cgatcaacaa cacatactcc tgtatgattg aaaatgacat tgccaaagca       240

acaggggnta tcaaagtgac agaatcggag atcaaaaggc ggagtcacct acagctgcta       300

aactcaaagg cttctctgtg tgtctcttct ttctttgcca tcagctgggc acttctgcct       360

ctcagccctt acctgatgct aanataatgt gccttggcca caaaaa                      406


<210>  13
<211>  462
<212>  DNA
<213>  Homo sapien

<400>  13
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atggcttccc tggggcagat cctcttctgg agcataatta gcatcatcat tattctggct       120

ggagcaattg cactcatcat tggctttggt atttcaggga gacactccat cacagtcact       180

actgtcgcct cagctgggaa cattggggag gatggaatcc tgagctgcac ttttgaacct       240

gacatcaaac tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc       300

catgagttca agaaggcaa agatgagctg tcggagcagg atgaaatgtt cagaggccgg       360

acagcagtgt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct gaaaaacgtg       420

caactcacag atgctggcac ctacaaatgt tatatcatca ct                          462
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<210>   14
<211>   272
<212>   DNA
<213>   Homo sapien

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ggcctcctcc agccagtgct gaccagggac ttctgacctg ctggccagcc aggacctgtg   120

tggggaggcc ctcctgctgc cttggggtga caatctcagc tccaggctac agggagaccg   180

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ggtgattctg gataaatact acttcctctg cg   272

<210>   15
<211>   492
<212>   PRT
<213>   Homo sapien

<400>   15

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
1   5   10   15

Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
                20   25   30

Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
            35   40   45

Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
        50   55   60

Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65   70   75   80

Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
                85   90   95

Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
                100   105   110

Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
            115   120   125

Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
        130   135   140

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Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145             150             155             160

Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
            165             170             175

Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
            180             185             190

Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
            195             200             205

Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
    210             215             220

Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225             230             235             240

Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
            245             250             255

Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
            260             265             270

Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
            275             280             285

Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
    290             295             300

Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305             310             315             320

Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
            325             330             335

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
            340             345             350

Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
            355             360             365

Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
    370             375             380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
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385                 390                 395                 400
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Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
              405   410   415

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
              420   425   430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
              435   440   445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
        450   455   460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465   470   475   480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
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<210>   16
<211>   890
<212>   DNA
<213>   Homo sapien

<220>
<221>   misc_feature
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<223>   n=a, c, g or t


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gcatctagag cagtgggact cagctggggt gatttcgccc cccatctccg ggggaatgtc     120

tgaagacaat tttggttacc tcaatgaggg agtggaggag gatacagnnn nnnnnnnnnn     180

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnncat     240

tacaactacc caatccgaag tgtcaactgt gtcaggacta agaaaccctg gttttgagta     300

gaaaagggcc tgggaaagag gggagccaac aaatctgtct gcttcctcac attagtcatt     360

ggcaaataag cattctgtct ctttggctgc tgcctcagca cagagagcca gaactctatc     420

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tgggattatc ttcagcttgt tgagcttcta gtttctttc ccttcattct accctgcaag     540

ccaagttctg taagagaaat gcctgagttc tagctcaggt tttcttactc tgaatttaga     600

tctccagacc ctgcctggcc acaattcaaa ttaaggcaac aaacatatac cttccatgaa     660
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gcacacacag acttttgaaa gcaaggacaa tgactgcttg aattgaggcc ttgaggaatg     720

aagctttgaa ggaaaagaat actttgtttc cagccccctt cccacactct tcatgtgtta     780

accactgcct tcctggacct tggagccacg gtgactgtat tacatgttgt tatagaaaac     840

tgattttaga gttctgatcg ttcaagagaa tgattaaata tacatttcct              890
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